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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,771

DATE: 07/26/2001
TIME: 15:20:52

Input Set : A:\203975US0X.txt
Output Set: N:\CRF3\07262001\I903771.raw

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  3 <110> APPLICANT: MOCKEL, Bettina
  4         KREUTZER, Caroline
  5         BATHE, Brigitte
  7 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE luxR GENE
  9 <130> FILE REFERENCE: 203975US0X
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/903,771
C--> 11 <141> CURRENT FILING DATE: 2001-07-13
 11 <150> PRIOR APPLICATION NUMBER: DE10039043.9
 12 <151> PRIOR FILING DATE: 2000-08-10
 14 <160> NUMBER OF SEQ ID NOS: 5
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1052
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Corynebacterium glutamicum
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (214)..(849)
 26 <223> OTHER INFORMATION:
 29 <400> SEQUENCE: 1
 30 tgcagcattg ccggtggagc caccagaggg gtttgtcggg cgccggtttt tggcagattc    60
 32 ggactcaagt gctacaggcg aggttgaact aagttctcca actgacgatg agtaaggcta   120
 34 gactaaagta cgattcatct gctcatcgat actcttgaag gcgcattttc attcgaaacg   180
 36 aagtgcgcca ttgggaagga cctagttcaa aca atg att cgc gtg ctg ctt gct   234
 37                                     Met Ile Arg Val Leu Leu Ala
 38                                       1               5
 40 gat gac cac gaa atc gtg agg ctc gga ctc cga gct gtg ctg gaa agc   282
 41 Asp Asp His Glu Ile Val Arg Leu Gly Leu Arg Ala Val Leu Glu Ser
 42         10              15              20
 44 gcc gag gac att gaa gtg gtg ggc gaa gtc tcc acc gcc gaa ggt gcg   330
 45 Ala Glu Asp Ile Glu Val Val Gly Glu Val Ser Thr Ala Glu Gly Ala
 46     25              30              35
 48 gtg cag gca gcc caa gaa ggc gga atc gac gtc atc ttg atg gac ctc   378
 49 Val Gln Ala Ala Gln Glu Gly Gly Ile Asp Val Ile Leu Met Asp Leu
 50 40              45              50              55
 52 cga ttc ggc ccc ggc gtc caa gga acc cag gtt tcc aca ggc gca gac   426
 53 Arg Phe Gly Pro Gly Val Gln Gly Thr Gln Val Ser Thr Gly Ala Asp
 54             60              65              70
 56 gcc acc gca gcc atc aag cga aac atc gat aac ccg cca aaa gtc ctg   474
 57 Ala Thr Ala Ala Ile Lys Arg Asn Ile Asp Asn Pro Pro Lys Val Leu
 58             75              80              85
 60 gtc gtg acc aac tac gac acc gac aca gac atc ctc ggc gca atc gaa   522
 61 Val Val Thr Asn Tyr Asp Thr Asp Thr Asp Ile Leu Gly Ala Ile Glu
 62         90              95              100
 64 gcc ggc gca ctg ggc tac ctg ctc aaa gac gcc cca ccg agc gaa ctc   570
 65 Ala Gly Ala Leu Gly Tyr Leu Leu Lys Asp Ala Pro Pro Ser Glu Leu
 66     105             110             115
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68 ctg gca gca gta cga tcc gca gca gaa ggt gac tcc aca ctg tca ccc        618
69 Leu Ala Ala Val Arg Ser Ala Ala Glu Gly Asp Ser Thr Leu Ser Pro
70 120                     125             130                 135
72 atg gtt gcg aac cgc ctg atg act cgc gtg cgc acc ccc aaa acc tca        666
73 Met Val Ala Asn Arg Leu Met Thr Arg Val Arg Thr Pro Lys Thr Ser
74             140                 145                 150
76 ctc acc cca cgt gaa ctg gaa gtt ctc aag ctg gtt gcc ggt gga tcc        714
77 Leu Thr Pro Arg Glu Leu Glu Val Leu Lys Leu Val Ala Gly Gly Ser
78             155                 160                 165
80 tcc aac cgc gac att ggc cgt atc ctc ttc ctc tca gaa gcc acg gtg        762
81 Ser Asn Arg Asp Ile Gly Arg Ile Leu Phe Leu Ser Glu Ala Thr Val
82         170                 175                 180
84 aaa tcc cac ctc gtg cac atc tac gac aag ctc ggc gtg cgg tca cgt        810
85 Lys Ser His Leu Val His Ile Tyr Asp Lys Leu Gly Val Arg Ser Arg
86     185                 190                 195
88 acc tcc gct gtc gca gcc gca cgt gag cag ggg ctg ctg tagcgggggt        859
89 Thr Ser Ala Val Ala Ala Ala Arg Glu Gln Gly Leu Leu
90 200                 205                 210
92 tgctgcaagg ctttaggtat ccgcgccggg gttggcctac gggagcatcc cgaggcttta     919
94 gcaggggcac gggctctggc ttgggctgag tcaggggcgc ggccaatgct ttccgacgcg     979
96 tgtctccacg gctttatta gtttttcaag aagtttgacg aaggtgcgta gatcctcttc     1039
98 gggccagtct gaa                                                         1052
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 212
103 <212> TYPE: PRT
104 <213> ORGANISM: Corynebacterium glutamicum
106 <400> SEQUENCE: 2
108 Met Ile Arg Val Leu Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly
109 1               5                   10                  15
112 Leu Arg Ala Val Leu Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu
113             20                  25                  30
116 Val Ser Thr Ala Glu Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile
117             35                  40                  45
120 Asp Val Ile Leu Met Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr
121     50                  55                  60
124 Gln Val Ser Thr Gly Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile
125 65                  70                  75                  80
128 Asp Asn Pro Pro Lys Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr
129                 85                  90                  95
132 Asp Ile Leu Gly Ala Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys
133             100                 105                 •110
136 Asp Ala Pro Pro Ser Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu
137         115                 120                 125
140 Gly Asp Ser Thr Leu Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg
141     130                 135                 140
144 Val Arg Thr Pro Lys Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu
145 145                 150                 155                 160
148 Lys Leu Val Ala Gly Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu
149                 165                 170                 175
```

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152 Phe Leu Ser Glu Ala Thr Val Lys Ser His Leu Val His Ile Tyr Asp
153             180             185             190
156 Lys Leu Gly Val Arg Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu
157         195             200             205
160 Gln Gly Leu Leu
161     210
164 <210> SEQ ID NO: 3
165 <211> LENGTH: 353
166 <212> TYPE: DNA
167 <213> ORGANISM: Corynebacterium glutamicum
169 <400> SEQUENCE: 3
170 ggaatcgacg tcatcttgat ggacctccga ttcggccccg gcgtccaagg aacccaggtt      60
172 tccacaggcg cagacgccac cgcagccatc aagcgaaaca tcgataaccc gccaaaagtc     120
174 ctggtcgtga ccaactacga caccgacaca gacatcctcg gcgcaatcga agccggcgca     180
176 ctgggctacc tgctcaaaga cgccccaccg agcgaactcc tggcagcagt acgatccgca     240
178 gcagaaggtg actccacact gtcacccatg gttgcgaacc gcctgatgac tcgcgtgcgc     300
180 accccaaaa cctcactcac cccacgtgaa ctggaagttc tcaagctggt tgc            353
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 20
185 <212> TYPE: DNA
186 <213> ORGANISM: Corynebacterium glutamicum
188 <400> SEQUENCE: 4                                                      20
189 ggaatcgacg tcatcttgat
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 20
194 <212> TYPE: DNA
195 <213> ORGANISM: Corynebacterium glutamicum
197 <400> SEQUENCE: 5                                                      20
198 gcaaccagct tgagaacttc
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VERIFICATION SUMMARY   DATE: 07/26/2001
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date